

BLAST

Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Protein Sequence (15 letters)

residues 66-80 of SEQ ID NO: 12

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

Icl|41354

Icl|41354

Description

None

Molecule type

amino acid

Query Length

15

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program

BLASTP 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Multiple alignment](#) [NEW](#)

Search Parameters

Program	blastp
Word size	2
Expect value	200000
Hitlist size	100
Gapcosts	9,1
Matrix	PAM30
Threshold	11
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date	Jan 3, 2010 5:44 PM
Number of letters	3,505,793,397
Number of sequences	10,274,250
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.358076	0.294
K	0.289736	0.11
H	1.81294	0.61

Results Statistics

Length adjustment	5
Effective length of query	10
Effective length of database	3454422147
Effective search space	34544221470
Effective search space used	34544221470

[Graphic Summary](#)

[Show Conserved Domains](#)

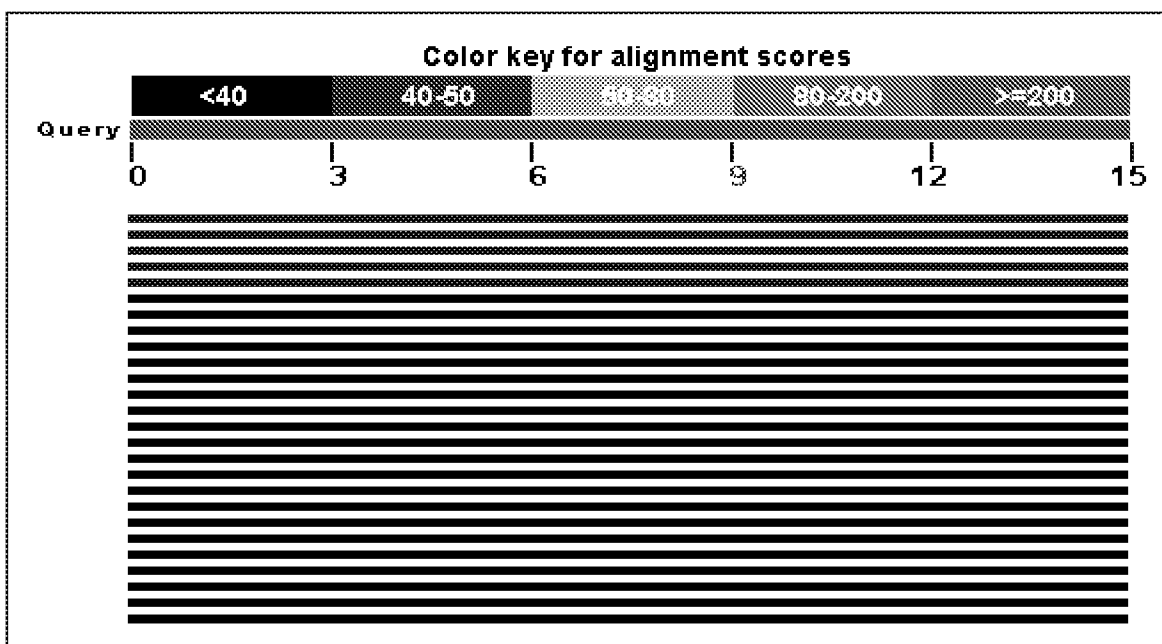
No putative conserved domains have been detected

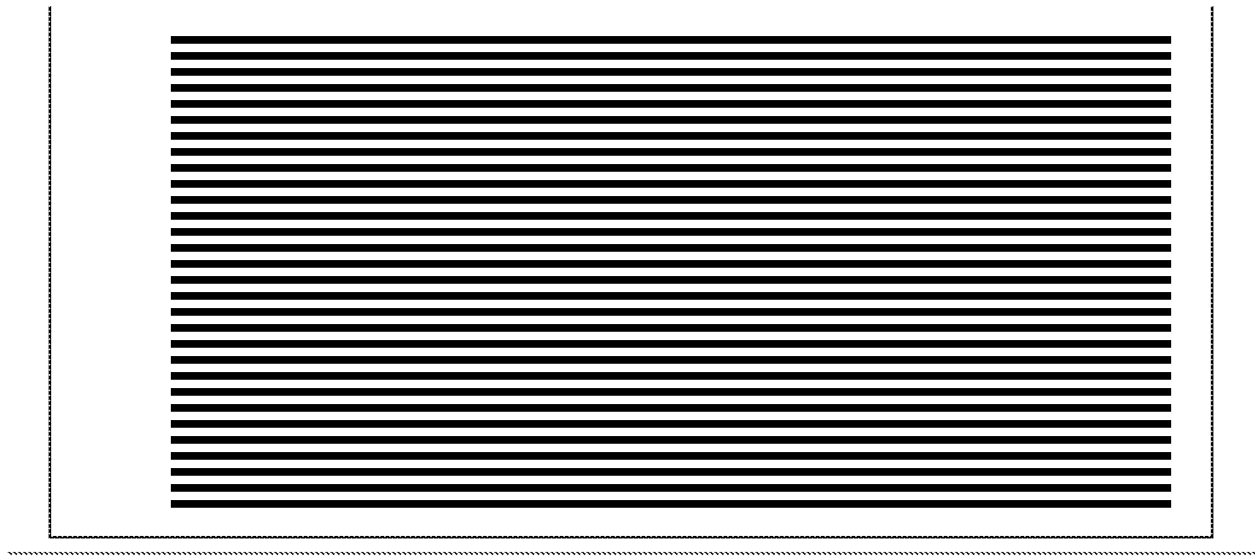


Distribution of 100 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





Descriptions

		Score	
E			
Sequences producing significant alignments:		(Bits)	Value
gb ABU97123.1	S protein [Hepatitis B virus]	43.5	0.003
gb ABI17005.1	surface antigen [Hepatitis B virus]	43.5	0.003
dbj BAG12008.1	S protein [Hepatitis B virus]	43.5	0.003
gb AAW65562.1	HBsAg [Hepatitis B virus]	43.5	0.003
gb AAD13661.1	surface antigen [Hepatitis B virus]	42.2	0.007
gb ACX36965.1	middle S protein [Hepatitis B virus] >gb ACX36...	39.7	0.040
gb ACX36957.1	middle S protein [Hepatitis B virus]	39.7	0.040
dbj BAG06746.1	hepatitis B surface antigen [Hepatitis B virus]	39.7	0.040
gb ACQ82752.1	S protein [Hepatitis B virus]	38.8	0.072
gb ACQ82751.1	middle S protein [Hepatitis B virus]	38.8	0.072
gb ACQ82750.1	large S protein [Hepatitis B virus]	38.8	0.072
dbj BAR84154.1	hepatitis B surface antigen [Hepatitis B virus]	38.8	0.072
dbj BAR84102.1	hepatitis B surface antigen [Hepatitis B virus]	38.8	0.072
dbj BAR83930.1	hepatitis B surface antigen [Hepatitis B virus]	38.8	0.072
gb ACJ66248.1	middle S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66247.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66242.1	S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66241.1	middle S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66240.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66233.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66228.1	S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66227.1	middle S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66226.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66213.1	middle S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66212.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66207.1	S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66206.1	middle S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66205.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66164.1	middle S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66163.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66136.1	middle S protein [Hepatitis B virus] >gb ACJ66...	38.8	0.072
gb ACJ66135.1	large S protein [Hepatitis B virus] >gb ACJ661...	38.8	0.072
gb ACJ66130.1	S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66129.1	middle S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66128.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66122.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66096.1	S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66095.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66091.1	large S protein [Hepatitis B virus] >gb ACJ660...	38.8	0.072
gb ACJ66006.1	S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66005.1	middle S protein [Hepatitis B virus]	38.8	0.072
gb ACJ66004.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACJ65907.1	middle S protein [Hepatitis B virus]	38.8	0.072
gb ACJ65906.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACJ65859.1	S protein [Hepatitis B virus]	38.8	0.072
gb ACJ65858.1	middle S protein [Hepatitis B virus]	38.8	0.072
gb ACJ65857.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACR66198.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACR66193.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACR66192.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACR66180.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACR66170.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACR66160.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACR66152.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACP66138.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACP66129.1	large S protein [Hepatitis B virus]	38.8	0.072
gb ACP66123.1	large S protein [Hepatitis B virus]	38.8	0.072

gb ACR66097.1	large S protein [Hepatitis B virus]	>gb ACR661...	38.8	0.072
gb ACR66094.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR66086.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR66020.1	large S protein [Hepatitis B virus]	>gb ACR660...	38.8	0.072
gb ACR66001.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR65984.1	large S protein [Hepatitis B virus]	>gb ACR661...	38.8	0.072
gb ACP65964.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP65943.1	large S protein [Hepatitis B virus]	>gb ACR659...	38.8	0.072
gb ACP65941.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR65932.1	large S protein [Hepatitis B virus]	>gb ACR660...	38.8	0.072
gb ACR65923.1	large S protein [Hepatitis B virus]	>gb ACR660...	38.8	0.072
gb ACR65920.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR65903.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR65891.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR65884.1	large S protein [Hepatitis B virus]	>gb ACR660...	38.8	0.072
gb ACR65880.1	large S protein [Hepatitis B virus]	>gb ACR660...	38.8	0.072
gb ACP65878.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP65869.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP65859.1	large S protein [Hepatitis B virus]	>gb ACR660...	38.8	0.072
gb ACR65855.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR65852.1	large S protein [Hepatitis B virus]	>gb ACR659...	38.8	0.072
gb ACR65840.1	large S protein [Hepatitis B virus]	>gb ACR660...	38.8	0.072
gb ACR65833.1	large S protein [Hepatitis B virus]	>gb ACR658...	38.8	0.072
gb ACR65825.1	large S protein [Hepatitis B virus]	>gb ACR658...	38.8	0.072
gb ACR65817.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR65809.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP65807.1	large S protein [Hepatitis B virus]	>gb ACR658...	38.8	0.072
gb ACP65704.1	S protein [Hepatitis B virus]		38.8	0.072
gb ACP60703.1	middle S protein [Hepatitis B virus]		38.8	0.072
gb ACP60700.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP20564.1	S protein [Hepatitis B virus]		38.8	0.072
gb ACP20563.1	middle S protein [Hepatitis B virus]		38.8	0.072
gb ACP20560.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP20413.1	S protein [Hepatitis B virus]		38.8	0.072
gb ACP20412.1	middle S protein [Hepatitis B virus]		38.8	0.072
gb ACP20411.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP20326.1	S protein [Hepatitis B virus]		38.8	0.072
gb ACP20325.1	middle S protein [Hepatitis B virus]		38.8	0.072
gb ACP20324.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP20320.1	S protein [Hepatitis B virus]		38.8	0.072
gb ACP20319.1	middle S protein [Hepatitis B virus]		38.8	0.072
gb ACP20318.1	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP20311.1	S protein [Hepatitis B virus]		38.8	0.072

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [NEW](#)

>gb|ABU97123.1| S protein [Hepatitis B virus]
Length=57

Score = 43.5 bits (95), Expect = 0.003
Identities = 14/15 (93%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

```
Query 1  PLIPGSTRITSTGQCK 15
        PLIPGST TSTGQCK
Sbjct 1  PLIPGSTTTTSTGQCK 15
```

>gb|ABI17005.1| surface antigen [Hepatitis B virus]
Length=57

Score = 43.5 bits (95), Expect = 0.003
Identities = 14/15 (93%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

```
Query 1  PLIPGSTRITSTGQCK 15
        PLIPGST TSTGQCK
```

Sbjct 1 PLIPGSTITTSTGQCK 15

>dbj|BAG12008.1| S protein [Hepatitis B virus]
Length=254

Score = 43.5 bits (95), Expect = 0.003
Identities = 14/15 (93%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSTGQCK 15
PLIPGST TSTGQCK
Sbjct 136 PLIPGSTITTSTGQCK 150

>gb|AAW65562.1| HBsAg [Hepatitis B virus]
Length=226

Score = 43.5 bits (95), Expect = 0.003
Identities = 14/15 (93%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSTGQCK 15
PLIPGST TSTGQCK
Sbjct 108 PLIPGSTITTSTGQCK 122

>gb|AAD13661.1| surface antigen [Hepatitis B virus]
Length=226

Score = 42.2 bits (92), Expect = 0.007
Identities = 13/15 (86%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSTGQCK 15
PLIPG+TRITSTG CK
Sbjct 108 PLIPGTTTSTGPK 122

>gb|ACX36965.1| middle S protein [Hepatitis B virus]
>gb|ACX36975.1| middle S protein [Hepatitis B virus]
Length=243

Score = 39.7 bits (86), Expect = 0.040
Identities = 13/15 (86%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSTGQCK 15
PL+PGST TSTGQCK
Sbjct 125 PLLPGSTITTSTGQCK 139

>gb|ACX36957.1| middle S protein [Hepatitis B virus]
Length=243

Score = 39.7 bits (86), Expect = 0.040
Identities = 13/15 (86%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSTGQCK 15
PL+PGST TSTGQCK
Sbjct 125 PLLPGSTITTSTGQCK 139

>dbj|BAG06746.1| hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 39.7 bits (86), Expect = 0.040
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSTGQCK 15
PLIPGST TSTG CK
Sbjct 69 PLIPGSTITTSTGXCK 83

>gb|ACQ82752.1| S protein [Hepatitis B virus]
Length=226

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSTGQCK 15
PLIPGST TSTG CK
Sbjct 108 PLIPGSTITTSTGPK 122

>**gb|ACQ82751.1|** middle S protein [Hepatitis B virus]
Length=281

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 163 PLIPGSTTTSTGPCK 177

>**gb|ACQ82750.1|** large S protein [Hepatitis B virus]
Length=400

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 282 PLIPGSTTTSTGPCK 296

>**dbj|BAH84154.1|** hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 69 PLIPGSTTTSTGPCK 83

>**dbj|BAH84102.1|** hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 69 PLIPGSTTTSTGPCK 83

>**dbj|BAH83930.1|** hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 69 PLIPGSTTTSTGPCK 83

>**gb|ACJ66248.1|** middle S protein [Hepatitis B virus]
Length=281

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 163 PLIPGSTTTSTGPCK 177

>**gb|ACJ66247.1|** large S protein [Hepatitis B virus]
Length=400

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 282 PLIPGSTTTSTGPCK 296

>**gb|ACJ66242.1|** S protein [Hepatitis B virus]
Length=226

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSTGQCK 15
PLIPGST TSTG CK
Sbjct 108 PLIPGSTTTTSTGPCK 122

>gb|ACJ66241.1| middle S protein [Hepatitis B virus]
Length=281

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSTGQCK 15
PLIPGST TSTG CK
Sbjct 163 PLIPGSTTTTSTGPCK 177

>gb|ACJ66240.1| large S protein [Hepatitis B virus]
Length=400

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSTGQCK 15
PLIPGST TSTG CK
Sbjct 282 PLIPGSTTTTSTGPCK 296

>gb|ACJ66233.1| large S protein [Hepatitis B virus]
Length=400

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSTGQCK 15
PLIPGST TSTG CK
Sbjct 282 PLIPGSTTTTSTGPCK 296

>gb|ACJ66228.1| S protein [Hepatitis B virus]
Length=226

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSTGQCK 15
PLIPGST TSTG CK
Sbjct 108 PLIPGSTTTTSTGPCK 122

>gb|ACJ66227.1| middle S protein [Hepatitis B virus]
Length=281

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSTGQCK 15
PLIPGST TSTG CK
Sbjct 163 PLIPGSTTTTSTGPCK 177

>gb|ACJ66226.1| large S protein [Hepatitis B virus]
Length=400

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSTGQCK 15
PLIPGST TSTG CK
Sbjct 282 PLIPGSTTTTSTGPCK 296

>gb|ACJ66213.1| middle S protein [Hepatitis B virus]
Length=281

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)


```
Query 1 PLIPGSTRSTGQCK 15
        PLIPGST TSTG CK
Sbjct 163 PLIPGSTTTSTGPCK 177
```

>**gb|ACJ66212.1|** large S protein [Hepatitis B virus]
Length=400

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

```
Query 1 PLIPGSTRSTGQCK 15
        PLIPGST TSTG CK
Sbjct 282 PLIPGSTTTSTGPCK 296
```

>**gb|ACJ66207.1|** S protein [Hepatitis B virus]
Length=226

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

```
Query 1 PLIPGSTRSTGQCK 15
        PLIPGST TSTG CK
Sbjct 108 PLIPGSTTTSTGPCK 122
```

>**gb|ACJ66206.1|** middle S protein [Hepatitis B virus]
Length=279

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

```
Query 1 PLIPGSTRSTGQCK 15
        PLIPGST TSTG CK
Sbjct 161 PLIPGSTTTSTGPCK 175
```

>**gb|ACJ66205.1|** large S protein [Hepatitis B virus]
Length=398

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

```
Query 1 PLIPGSTRSTGQCK 15
        PLIPGST TSTG CK
Sbjct 280 PLIPGSTTTSTGPCK 294
```

>**gb|ACJ66164.1|** middle S protein [Hepatitis B virus]
Length=281

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

```
Query 1 PLIPGSTRSTGQCK 15
        PLIPGST TSTG CK
Sbjct 163 PLIPGSTTTSTGPCK 177
```

>**gb|ACJ66163.1|** large S protein [Hepatitis B virus]
Length=400

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

```
Query 1 PLIPGSTRSTGQCK 15
        PLIPGST TSTG CK
Sbjct 282 PLIPGSTTTSTGPCK 296
```

>**gb|ACJ66136.1|** middle S protein [Hepatitis B virus]
gb|ACJ66178.1| middle S protein [Hepatitis B virus]
gb|ACJ66192.1| middle S protein [Hepatitis B virus]
gb|ACJ66198.1| middle S protein [Hepatitis B virus]
Length=281

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 163 PLIPGSTTTSTGPCK 177

>gb|ACJ66135.1| large S protein [Hepatitis B virus]
gb|ACJ66177.1| large S protein [Hepatitis B virus]
gb|ACJ66191.1| large S protein [Hepatitis B virus]
gb|ACJ66203.1| large S protein [Hepatitis B virus]
Length=400

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ66130.1| S protein [Hepatitis B virus]
Length=226

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 108 PLIPGSTTTSTGPCK 122

>gb|ACJ66129.1| middle S protein [Hepatitis B virus]
Length=281

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 163 PLIPGSTTTSTGPCK 177

>gb|ACJ66128.1| large S protein [Hepatitis B virus]
Length=400

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ66122.1| large S protein [Hepatitis B virus]
Length=400

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ66096.1| S protein [Hepatitis B virus]
Length=226

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 108 PLIPGSTTTSTGPCK 122

>gb|ACJ66095.1| large S protein [Hepatitis B virus]
Length=400

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ66081.1| large S protein [Hepatitis B virus]
gb|ACJ66088.1| large S protein [Hepatitis B virus]
gb|ACJ66142.1| large S protein [Hepatitis B virus]
gb|ACJ66156.1| large S protein [Hepatitis B virus]
Length=400

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ66006.1| S protein [Hepatitis B virus]
Length=226

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 108 PLIPGSTTTSTGPCK 122

>gb|ACJ66005.1| middle S protein [Hepatitis B virus]
Length=281

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 163 PLIPGSTTTSTGPCK 177

>gb|ACJ66004.1| large S protein [Hepatitis B virus]
Length=400

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ65907.1| middle S protein [Hepatitis B virus]
Length=281

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 163 PLIPGSTTTSTGPCK 177

>gb|ACJ65906.1| large S protein [Hepatitis B virus]
Length=400

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ65859.1| S protein [Hepatitis B virus]
Length=226

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

```
Query 1 PLIPGSTRSTGQCK 15
        PLIPGST TSTG CK
Sbjct 108 PLIPGSTTTSTGPCK 122
```

>**gb|ACJ65858.1|** middle S protein [Hepatitis B virus]
Length=281

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

```
Query 1 PLIPGSTRSTGQCK 15
        PLIPGST TSTG CK
Sbjct 163 PLIPGSTTTSTGPCK 177
```

>**gb|ACJ65857.1|** large S protein [Hepatitis B virus]
Length=400

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

```
Query 1 PLIPGSTRSTGQCK 15
        PLIPGST TSTG CK
Sbjct 282 PLIPGSTTTSTGPCK 296
```

>**gb|ACR66198.1|** large S protein [Hepatitis B virus]
Length=215

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

```
Query 1 PLIPGSTRSTGQCK 15
        PLIPGST TSTG CK
Sbjct 120 PLIPGSTTTSTGPCK 134
```

>**gb|ACR66183.1|** large S protein [Hepatitis B virus]
Length=215

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

```
Query 1 PLIPGSTRSTGQCK 15
        PLIPGST TSTG CK
Sbjct 120 PLIPGSTTTSTGPCK 134
```

>**gb|ACR66182.1|** large S protein [Hepatitis B virus]
Length=215

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

```
Query 1 PLIPGSTRSTGQCK 15
        PLIPGST TSTG CK
Sbjct 120 PLIPGSTTTSTGPCK 134
```

>**gb|ACR66180.1|** large S protein [Hepatitis B virus]
Length=215

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

```
Query 1 PLIPGSTRSTGQCK 15
        PLIPGST TSTG CK
Sbjct 120 PLIPGSTTTSTGPCK 134
```

>**gb|ACR66170.1|** large S protein [Hepatitis B virus]
Length=215

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

```
Query 1 PLIPGSTRSTGQCK 15
        PLIPGST TSTG CK
```

Sbjct 120 PLIPGSTTTSTGPCK 134

>**gb|ACR66160.1|** large S protein [Hepatitis B virus]
Length=215

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 120 PLIPGSTTTSTGPCK 134

>**gb|ACR66152.1|** large S protein [Hepatitis B virus]
Length=215

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 120 PLIPGSTTTSTGPCK 134

>**gb|ACR66138.1|** large S protein [Hepatitis B virus]
Length=215

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 120 PLIPGSTTTSTGPCK 134

>**gb|ACR66129.1|** large S protein [Hepatitis B virus]
Length=215

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 120 PLIPGSTTTSTGPCK 134

>**gb|ACR66123.1|** large S protein [Hepatitis B virus]
Length=215

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 120 PLIPGSTTTSTGPCK 134

>**gb|ACR66097.1|** large S protein [Hepatitis B virus]
gb|ACR66110.1| large S protein [Hepatitis B virus]
Length=215

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 120 PLIPGSTTTSTGPCK 134

>**gb|ACR66094.1|** large S protein [Hepatitis B virus]
Length=215

Score = 38.8 bits (84), Expect = 0.072
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15
PLIPGST TSTG CK
Sbjct 120 PLIPGSTTTSTGPCK 134